63. The method of claim **53**, wherein the ligating comprises ligating to an overhang or a blunt end.

64. The method of claim **53**, further comprising detecting mutations in one or more of the error-corrected sequences as compared to a reference sequence.

65. The method of claim **53**, wherein sequencing the cypher-target amplification products comprises converting data from a sequencing instrument into quality scores and then into sequencing reads.

66. The method of claim **53**, further comprising purifying a plurality of cypher-target nucleic acid complexes prior to sequencing, wherein the purified cypher-target nucleic acid complexes comprise nucleic acid molecules from specific genomic regions.

67. The method of claim **53**, wherein the plurality of circulating DNA molecules comprise a mutation present at a frequency of 2.1×10^{-6} or lower.

68. The method of claim **53**, wherein generating the error corrected sequences results in a measureable sequencing error rate from about 10^{-6} to about 10^{-8}.

69. The method of claim **53**, wherein the circulating DNA molecules comprise plasma DNA biomarkers.

70. The method of claim **53**, wherein each identifier tag of the plurality of distinct identifier tag sequences is a random or partially random sequence of about 5 nucleotides in length.

71. The method of claim **53**, wherein each identifier tag of the plurality of distinct identifier tag sequences is a random or partially random sequence of 5 or 6 nucleotides in length.

72. The method of claim **53**, wherein the cypher polynucleotides comprising the identifier tags are contained within a pool of cypher polynucleotides comprising known sequences.

73. The method of claim **53**, wherein the ligating comprises ligating identifier tags to both ends of the circulating DNA molecules, and further wherein the identifier tags at both ends together form a unique pair of identifiers that differ between each of the other pairs of identifiers ligated to the circulating DNA molecules.

74. The method of claim **53**, wherein grouping sequencing reads is based on (i) the identifier tag sequence and (ii) sequence information from an end of the circulating DNA molecule.

75. The method of claim **61**, further comprising purifying a plurality of cypher-target nucleic acid complexes prior to sequencing, wherein the purified cypher-target nucleic acid complexes comprise nucleic acid molecules from specific genomic regions.

76. The method of claim **61**, further comprising identifying one or more single nucleotide mutations.

77. The method of claim **61**, wherein the circulating DNA molecules comprise blood biomarkers.

78. The method of claim **61**, wherein the circulating DNA molecules comprise DNA molecules derived from cancer cells.

79. The method of claim **61**, wherein each identifier tag of the plurality of distinct identifier tag sequences is a random or partially random sequence of about 5 nucleotides in length.

80. The method of claim **61**, wherein each identifier tag of the plurality of distinct identifier tag sequences is a random or partially random sequence of 5 or 6 nucleotides in length.

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